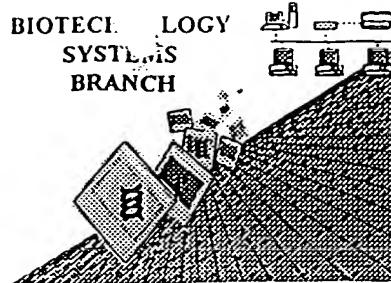


RAW SEQUENCE LISTING

ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/899,824

Source: OTPE

Date Processed by STIC: 7/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

Does Not Comply
Corrected Diskette Needed
see Add 1

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 109/899,569

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,569

DATE: 07/20/2001

TIME: 14:20:30

Input Set : A:\0652 2280001 seq list.txt
 Output Set: N:\CRF3\07202001\I899569.raw

```

4 <110> APPLICANT: Schweifer, Norbert
5      Scherl-Mostageer, Marwa
6      Sommergruber, Wolfgang
7      Abseher, Roger
9 <120> TITLE OF INVENTION: Tumorassoziiertes Antigen (B345)
11 <130> FILE REFERENCE: 0652.2280001/EKS/AES
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/899,569
C--> 14 <141> CURRENT FILING DATE: 2001-07-06
16 <150> PRIOR APPLICATION NUMBER: DE 100 33 080.0
17 <151> PRIOR FILING DATE: 2000-07-07
19 <150> PRIOR APPLICATION NUMBER: DE 101 19 294.0
20 <151> PRIOR FILING DATE: 2001-04-19
22 <150> PRIOR APPLICATION NUMBER: US 60/243,158
23 <151> PRIOR FILING DATE: 2000-10-25
25 <150> PRIOR APPLICATION NUMBER: US 60/297,747
26 <151> PRIOR FILING DATE: 2001-06-14
28 <160> NUMBER OF SEQ ID NOS: 40
30 <170> SOFTWARE: PatentIn Ver. 2.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 5897
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
40 <221> NAME/KEY: 5'UTR
41 <222> LOCATION: (1)..(214)
43 <220> FEATURE:
44 <221> NAME/KEY: CDS
45 <222> LOCATION: (215)..(2464)
47 <220> FEATURE:
48 <221> NAME/KEY: 3'UTR
49 <222> LOCATION: (2465)..(5897)
51 <400> SEQUENCE: 1
52 cttgagatat tagaattcgc gactcctgaa ctgcgggtc tctatcgac tgctagggt 60
54 tctgctgctg ggtgcggcgc gcctgcccg cgccccagaa gcttttgaga ttgcctgccc 120
56 acgagaaaagc aacattacag ttctcataaaa gctggggacc ccgactctgc tggccaaaacc 180
58 ctgttacatc gtcatttcta aaagacatata aacc atg ttg tcc atc aag tct gga 235
59                               Met Leu Ser Ile Lys Ser Gly
60                               1           5
62 gaa aga ata gtc ttt acc ttt agc tgc cag agt cct gag aat cac ttt 283
63 Glu Arg Ile Val Phe Thr Phe Ser Cys Gln Ser Pro Glu Asn His Phe
64      10          15          20
66 gtc ata gag atc cag aaa aat att gac tgt atg tca ggc cca tgt cct 331
67 Val Ile Glu Ile Gln Lys Asn Ile Asp Cys Met Ser Gly Pro Cys Pro
68      25          30          35
70 ttt ggg gag gtt cag ctt cag ccc tcg aca tcg ttg ttg cct acc ctc 379
71 Phe Gly Glu Val Gln Leu Gln Pro Ser Thr Ser Leu Leu Pro Thr Leu
72      40          45          50          55

```

Does Not Comply
 Corrected Diskette Needed
See Add 1

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,569

DATE: 07/20/2001

TIME: 14:20:30

Input Set : A:\0652 2280001 seq list.txt

Output Set: N:\CRF3\07202001\I899569.raw

75	aac aga act ttc atc tgg gat gtc aaa gct cat aag agc atc ggt tta	427
76	Asn Arg Thr Phe Ile Trp Asp Val Lys Ala His Lys Ser Ile Gly Leu	
77	60 65 70	
79	gag ctg cag ttt tcc atc cct cgc ctg agg cag atc ggt ccg ggt gag	475
80	Glu Leu Gln Phe Ser Ile Pro Arg Leu Arg Gln Ile Gly Pro Gly Glu	
81	75 80 85	
83	agc tgc cca gac gga gtc act cac tcc atc agc ggc cga atc gat gcc	523
84	Ser Cys Pro Asp Gly Val Thr His Ser Ile Ser Gly Arg Ile Asp Ala	
85	90 95 100	
87	acc gtg gtc agg atc gga acc ttc tgc agc aat ggc act gtg tcc cgg	571
88	Thr Val Val Arg Ile Gly Thr Phe Cys Ser Asn Gly Thr Val Ser Arg	
89	105 110 115	
91	atc aag atg caa gaa gga gtg aaa atg gcc tta cac ctc cca tgg ttc	619
92	Ile Lys Met Gln Glu Gly Val Lys Met Ala Leu His Leu Pro Trp Phe	
93	120 125 130 135	
95	cac ccc aga aat gtc tcc ggc ttc agc att gca aac cgc tca tct ata	667
96	His Pro Arg Asn Val Ser Gly Phe Ser Ile Ala Asn Arg Ser Ser Ile	
97	140 145 150	
99	aaa cgt ctg tgc atc atc gag tct gtg ttt gag ggt gaa ggc tca gca	715
100	Lys Arg Leu Cys Ile Ile Glu Ser Val Phe Glu Gly Glu Gly Ser Ala	
101	155 160 165	
103	acc ctg atg tct gcc aac tac cca gaa ggc ttc cct gag gat gag ctc	763
104	Thr Leu Met Ser Ala Asn Tyr Pro Glu Gly Phe Pro Glu Asp Glu Leu	
105	170 175 180	
107	atg acg tgg cag ttt gtc gtt cct gca cac ctg cgg gcc agc gtc tcc	811
108	Met Thr Trp Gln Phe Val Val Pro Ala His Leu Arg Ala Ser Val Ser	
109	185 190 195	
111	tcc ctc aac ttc aac ctc tcc aac tgt gag agg aag gag gag cgg gtt	859
112	Phe Leu Asn Phe Asn Leu Ser Asn Cys Glu Arg Lys Glu Glu Arg Val	
113	200 205 210 215	
115	gaa tac tac atc ccg ggc tcc acc acc aac ccc gag gtg ttc aag ctg	907
116	Glu Tyr Tyr Ile Pro Gly Ser Thr Thr Asn Pro Glu Val Phe Lys Leu	
117	220 225 230	
119	gag gac aag cag cct ggg aac atg gcg ggg aac ttc aac ctc tct ctg	955
120	Glu Asp Lys Gln Pro Gly Asn Met Ala Gly Asn Phe Asn Leu Ser Leu	
121	235 240 245	
123	caa ggc tgt gac caa gat gcc caa agt cca ggg atc ctc cgg ctg cag	1003
124	Gln Gly Cys Asp Gln Asp Ala Gln Ser Pro Gly Ile Leu Arg Leu Gln	
125	250 255 260	
127	ttc caa gtt ttg gtc caa cat cca caa aat gaa agc aat aaa atc tac	1051
128	Phe Gln Val Leu Val Gln His Pro Gln Asn Glu Ser Asn Lys Ile Tyr	
129	265 270 275	
133	gtg gtt gac ttg agt aat gag cga gcc atg tca ctc acc atc gag cca	1099
134	Val Val Asp Leu Ser Asn Glu Arg Ala Met Ser Leu Thr Ile Glu Pro	
135	280 285 290 295	
137	cgg ccc gtc aaa cag agc cgc aag ttt gtc cct ggc tgt ttc gtg tgt	1147
138	Arg Pro Val Lys Gln Ser Arg Lys Phe Val Pro Gly Cys Phe Val Cys	
139	300 305 310	
142	cta gaa tct cgg acc tgc agt agc aac ctc acc ctg aca tct ggc tcc	1195

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,569

DATE: 07/20/2001

TIME: 14:20:30

Input Set : A:\0652 2280001 seq list.txt
 Output Set: N:\CRF3\07202001\I899569.raw

143	Leu	Glu	Ser	Arg	Thr	Cys	Ser	Ser	Asn	Leu	Thr	Leu	Thr	Ser	Gly	Ser			
144										315		320					325		
146	aaa	cac	aaa	atc	tcc	ttc	ctt	tgt	gat	gat	ctg	aca	cgt	ctg	tgg	atg		1243	
147	Lys	His	Lys	Ile	Ser	Phe	Leu	Cys	Asp	Asp	Leu	Thr	Arg	Leu	Trp	Met			
148										330		335					340		
150	aat	gtg	gaa	aaa	acc	ata	agc	tgc	aca	gac	cac	cg	ta	c	tg	caa	agg		1291
151	Asn	Val	Glu	Lys	Thr	Ile	Ser	Cys	Thr	Asp	His	Arg	Tyr	Cys	Gln	Arg			
152										345		350					355		
154	aaa	tcc	tac	tca	ctc	cag	gtg	ccc	agt	gac	atc	ctc	cac	ctg	cct	gtg		1339	
155	Lys	Ser	Tyr	Ser	Leu	Gln	Val	Pro	Ser	Asp	Ile	Leu	His	Leu	Pro	Val			
156										360		365					370		375
158	gag	ctg	cat	gac	tcc	tcc	tgg	aag	ctg	ctg	gtg	ccc	aag	gac	agg	ctc		1387	
159	Glu	Leu	His	Asp	Phe	Ser	Trp	Lys	Leu	Leu	Val	Pro	Lys	Asp	Arg	Leu			
160										380		385					390		
162	agc	ctg	gtg	ctg	gtg	cca	gcc	cag	aag	ctg	cag	cag	cat	aca	cac	gag		1435	
163	Ser	Leu	Val	Leu	Val	Pro	Ala	Gln	Lys	Leu	Gln	Gln	His	Thr	His	Glu			
164										395		400					405		
166	aag	ccc	tgc	aac	acc	agc	tcc	atc	gtg	gcc	agt	gcc	ata	ccc				1483	
167	Lys	Pro	Cys	Asn	Thr	Ser	Phe	Ser	Tyr	Leu	Val	Ala	Ser	Ala	Ile	Pro			
168										410		415					420		
170	agc	cag	gac	ctg	tac	tcc	ggc	tcc	tcc	tgc	ccg	gga	ggc	tct	atc	aag		1531	
171	Ser	Gln	Asp	Leu	Tyr	Phe	Gly	Ser	Phe	Cys	Pro	Gly	Gly	Ser	Ile	Lys			
172										425		430					435		
174	cag	atc	cag	gtg	aag	cag	aac	atc	tcg	gtg	acc	ctt	cg	acc	ttt	gcc		1579	
175	Gln	Ile	Gln	Val	Lys	Gln	Asn	Ile	Ser	Val	Thr	Leu	Arg	Thr	Phe	Ala			
176										440		445					450		455
178	ccc	agc	tcc	caa	caa	gag	gcc	tcc	agg	cag	ggt	ctg	acg	gtg	tcc	ttt		1627	
179	Pro	Ser	Phe	Gln	Gln	Glu	Ala	Ser	Arg	Gln	Gly	Leu	Thr	Val	Ser	Phe			
180										460		465					470		
182	ata	cct	tat	tcc	aaa	gag	gaa	ggc	gtt	tcc	acg	gtg	acc	cct	gac	aca		1675	
183	Ile	Pro	Tyr	Phe	Lys	Glu	Glu	Gly	Val	Phe	Thr	Val	Thr	Pro	Asp	Thr			
184										475		480					485		
186	aaa	agc	aag	gtc	tac	ctg	agg	acc	ccc	aac	tgg	gac	cg	gg	ctg	cca		1723	
187	Lys	Ser	Lys	Val	Tyr	Leu	Arg	Thr	Pro	Asn	Trp	Asp	Arg	Gly	Leu	Pro			
188										490		495					500		
191	tcc	ctc	acc	tct	gtg	tcc	tgg	aac	atc	agc	gtg	ccc	aga	gac	cag	gtg		1771	
192	Ser	Leu	Thr	Ser	Val	Ser	Trp	Asn	Ile	Ser	Val	Pro	Arg	Asp	Gln	Val			
193										505		510					515		
195	gcc	tgc	ctg	act	tcc	ttt	aag	gag	cg	agc	ggc	gtg	gtc	tgc	cag	aca		1819	
196	Ala	Cys	Leu	Thr	Phe	Phe	Lys	Glu	Arg	Ser	Gly	Val	Val	Cys	Gln	Thr			
197										520		525					530		535
199	ggg	cgc	gca	tcc	atg	atc	atc	cag	gag	cag	cg	acc	cg	gct	gag	gag		1867	
200	Gly	Arg	Ala	Phe	Met	Ile	Ile	Gln	Glu	Gln	Arg	Thr	Arg	Ala	Glu	Glu			
201										540		545					550		
203	atc	tcc	atc	gtc	gac	gag	gat	gtg	ctc	ccc	aag	cca	agc	tcc	cac	cat		1915	
204	Ile	Phe	Ser	Leu	Asp	Glu	Asp	Val	Leu	Pro	Lys	Pro	Ser	Phe	His	His			
205										555		560					565		
207	cac	agc	tcc	tgg	gtc	aac	atc	tct	aac	tgc	agc	ccc	acg	agc	ggc	aag		1963	
208	His	Ser	Phe	Trp	Val	Asn	Ile	Ser	Asn	Cys	Ser	Pro	Thr	Ser	Gly	Lys			

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,569

DATE: 07/20/2001

TIME: 14:20:30

Input Set : A:\0652 2280001 seq list.txt
 Output Set: N:\CRF3\07202001\I899569.raw

209	570	575	580	
211	cag cta gac ctg ctc ttc tcg gtg aca ctt acc cca agg act gtg gac			2011
212	Gln Leu Asp Leu Leu Phe Ser Val Thr Leu Thr Pro Arg Thr Val Asp			
213	585	590	595	
215	ttg act gtc atc ctc atc gca gcg gtg gga ggt gga gtc tta ctg ctg			2059
216	Leu Thr Val Ile Leu Ile Ala Ala Val Gly Gly Val Leu Leu Leu			
217	600	605	610	615
219	tct gcc ctc ggg ctc atc att tgc tgt gtg aaa aag aag aaa aag aag			2107
220	Ser Ala Leu Gly Leu Ile Ile Cys Cys Val Lys Lys Lys Lys Lys			
221	620	625	630	
223	aca aac aag ggc ccc gct gtg ggt atc tac aat ggc aac atc aat act			2155
224	Thr Asn Lys Gly Pro Ala Val Gly Ile Tyr Asn Gly Asn Ile Asn Thr			
225	635	640	645	
227	gag atg cca ggc agc caa aaa agt ttc aga aag ggc gaa agg aca atg			2203
228	Glu Met Pro Gly Ser Gln Lys Ser Phe Arg Lys Gly Glu Arg Thr Met			
229	650	655	660	
231	act ccc atg tgt atg cag tca tcg agg aca cca tgg tat atg ggc atc			2251
232	Thr Pro Met Cys Met Gln Ser Ser Arg Thr Pro Trp Tyr Met Gly Ile			
233	665	670	675	
235	tgc tac agg att cca gcg gct cct tcc tgc agc cag agg tgg aca cct			2299
236	Cys Tyr Arg Ile Pro Ala Ala Pro Ser Cys Ser Gln Arg Trp Thr Pro			
237	680	685	690	695
239	acc ggc cgt tcc agg gca cca tgg ggg tct gtc ctc cct ccc cac cca			2347
240	Thr Gly Arg Ser Arg Ala Pro Trp Gly Ser Val Leu Pro Pro His Pro			
241	700	705	710	
243	cca tat gct cca ggg ccc caa ctg caa agt tgg cca ctg agg agc cac			2395
244	Pro Tyr Ala Pro Gly Pro Gln Leu Gln Ser Trp Pro Leu Arg Ser His			
245	715	720	725	
249	ctc ctc gct ccc ctc ctg agt ctg aga gtg aac cgt aca cct tct ccc			2443
250	Leu Leu Ala Pro Leu Leu Ser Leu Arg Val Asn Arg Thr Pro Ser Pro			
251	730	735	740	
253	atc cca aca atg ggg atg taa gcagcaagga cacagacatt cccttactga			2494
254	Ile Pro Thr Met Gly Met			
W--> 255	745	750	remove	
257	acactcagga gcccattggag cc agcagaat aacttgatcc attccagacg ctttgcttag			2554
259	tttcataaag cagggcactg agacaccgt ccgtgttctt aaccagaaaat cctaaagaag			2614
261	aggaaattata cagaaggaac agcaggaggt ttccctggac accgccaact tcacattgct			2674
263	cagtggactc attctaaggg caagacattt aaaatgtatca attccaatct ggatacagtc			2734
265	atgacagctc atgtgtctt caacttaggc tgtgcgttca gccagctgt aatgagagga			2794
267	gagaggcctg agtcacccatg catagggtt cagcaagccc tggattcaga gtgttaaaca			2854
269	gaggccttgc ctcttcagga caacagtttca aatttcaagg agccttacctg aggtccctac			2914
271	tctcacttggg gtccccagga tgaaaacgac aatgtgcctt tttatttata tttattttgt			2974
273	ggtccctgtt tatttaagag atcaaatgtt taaccaccta gcttttca cctgacttag			3034
275	taataactca tactaactgg tttggatgcc tgggttgta cttctactga ccgcttagata			3094
277	aacgtgtgcc tgtccccag gtgggtggaa taatttacaa tctgtccaaac cagaaaaagaa			3154
279	tgtgtgtgt tgagcagcat tgacacatat ctgcgttcat aagagacttc ctgattctct			3214
281	aggctcggttc gtggttatcc cattgtggaa attcatctt aatcccattt tcctatagtc			3274
283	ctagcaataa gagaaatttc ctcaagtttca catgtgcgt ttcctactgt gcagcaatac			3334
285	tttgcacattt aaagagaaat ttagagaata ttctcatcct ctaaaaatgt taaaatatat			3394

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,569

DATE: 07/20/2001

TIME: 14:20:30

Input Set : A:\0652 2280001 seq list.txt
 Output Set: N:\CRF3\07202001\I899569.raw

287 accaaacagt ggccccctgc attagtttc tggccact gcaaccatt acttggtagc 3454
 289 taaaaaaca cacattagct tatagtcctg gggatcagaa ttccaaaatg gatgtccctg 3514
 291 aatgaaaatc aagggtgtcag cagagctgtg ctccctctga aggctctagg gagaagccgg 3574
 293 ttccctgcctt tttcaagctt ctagaggctg gtcattcc caggctccag tggctggta 3634
 295 agctttctc acatggcatc actgtgacac tggccctccc acttccctct ttgacttaca 3694
 297 aagcccacca ggaagatcca ggataatctc tccatctaaa gatccttcat catcctggaa 3754
 299 gagccttttg ccatgcaaga caacatagcc acaggtgggg attaggacca ggacatctt 3814
 301 ggggtgctgt tatttcgcctt accacacccctt cctgcccacbg actcccacag gagaggctac 3874
 303 aaaatgatct ggcgcacagg gatgttttgtt ttagcttgcg gactctaaca cttaaaaaaa 3934
 305 ccccagatca gaagatctgg ccattgtggg gtcacattc tcaccttagca acaactggct 3994
 307 ggagctgggc accagctctg cctttagaaag ggggttccac ttccaccaggc caccacagcc 4054
 309 cacactacgc cctatcactt cccacaatga ggctaagtgt ttgtttctac tgatcaatgc 4114
 311 ccctgcaggt tgcattttt gtaatgaaaa agaaagactg ggattaatct ctaatcaggt 4174
 313 gagtagacca tgagaccaat gtgtgctcac attacccttt ttctttttt tcttttctt 4234
 315 tttttttttttttttagt gagacagat ctcattctgt tgccctaggct ggagtgcagt 4294
 317 ggcgcaatct cggctcactg caacctctgc ctccctggct caagcaattc tcccacctca 4354
 319 gcctcccaa tagctggat cactggcaca aaccaccatg cccagctaattttt 4414
 321 ttgttagagac agggtttac catgttggcc aggctgtct caacctcctg ggctcaagca 4474
 323 atcctcctgc ctcggcctcc caaagtgtcggg ggattacaga tggccac cgcacccagc 4534
 325 cccacaccct catttatacc aattacctgc ccagtaactg tggacttttgccttccacc 4594
 327 cctgctctga tctgaaagga gagggattat gttatagctt gtcagcacag tcccaagttc 4654
 329 aatatttctg cggccaaaaac ttcccttcaaa aaataaatgt acttcattgtt attcaatgaa 4714
 331 ttcaccttgg aaatgcacccg cctcaacttgc ttcacatggc ataaatgaaa ggaattttat 4774
 333 agtctcctaa atggcggtgtt ctgcaagacc tcttgaacac ttcccgagg ataggatatt 4834
 335 taagtcatgc ccttggcggtt gcctatggca cctttccctt ctgaaagtct gttccctgcc 4894
 337 cagtgaccct tggccttgc tggccatggc agccgatgt ctgaccctgc ataaaggccc 4954
 339 tgcggcttcc ttccctcactt gaagagccct tatttgaattt cactgtgtgg agccctagcc 5014
 341 ctccatttcc gacattcccc aacctcccg ccccttccaa gcaggactatg gtgcctgc 5074
 343 ttccacccaa ggtggatttgc ctcccttgc ggtggctac ttgtcaccat caccgacatc 5134
 345 actgttgcct gcaaggacac cacgtggca tttcccttca actgaggctt caaaactcct 5194
 347 ggacaaagtttgc ctggctcttgc agaccatgtt ttcctggagm tggccctcag tgaagggcc 5254
 349 cagccctgagg aaccctggctt ttttcttta aagcccaggc cccacttaca taaaacattt 5314
 W--> 351 cagggtaactt ggaacacgtt aagtggccatt tggtaagcc tacttgcatac cagccactg 5374
 W--> 353 ctcatccacg tggatgttgc tgcctacagc gaaggccacg gcatgcacgg atggctctca 5434
 W--> 355 atgtgtgtt cattgcacag aaggaaagg tctcaaggaa gatgtcaactg ggacaagcac 5494
 357 aagccacccg gacatggcc tggtaaaggat tagcagactg gtgtgtgtgg atctgcagt 5554
 359 cttcaacttgc aataattttt tcattgcaga tacttttttgc tggcattttt attcattcc 5614
 361 tgtgtttaa ataaacaaat gtaccaaaaa acaagtatca agtgcattaa gtgcctccggc 5674
 363 tacttgtccc ctgggtcagt agaggccccg gtttccctgt tggactgt gacaggctca 5734
 365 gcatgggctc agcagatgtt gtcattttt gttgatgata cagaaagcca ggcttggga 5794
 367 tacaagtctt ttccttca tttgatggc tgcactgtgtt gaaacatgtt ttttgcctt 5854
 369 gaaataaaaaa taatgtctt ggagtctcgc caaaaaaaaaa aag 5897
 373 <210> SEQ ID NO: 2
 374 <211> LENGTH: 749
 375 <212> TYPE: PRT
 376 <213> ORGANISM: Homo sapiens
 378 <400> SEQUENCE: 2
 379 Met Leu Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe Ser Cys
 380 1 5 10 15

See item
Number 9 on
ERROR Summary
Sheet

<210> 38
 <211> 23
 <212> DNA
 <213> Kunstliche Sequenz

<220>
 <221> 5'UTR
 <222> (1) .. (282)

<220>
 <221> GC_signal
 <222> (147) .. (157)

<220>
 <221> misc_feature
 <222> (201) .. (209)
 <223> cap signal; Transkriptionsstart

<220>
 <221> 3'UTR
 <222> (2794) .. (6163)

<220>
 <221> 3'UTR
 <222> (2794) .. (6163)

<220>
 <221> CDS
 <222> (283) .. (2793)

<400> 38
 agcagcagaa ccccttagcag tgc

The ranges provided
 for numeric identifiers
 <222> are larger than
 the actual sequence.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/899,569

DATE: 07/20/2001

TIME: 14:20:31

Input Set : A:\0652 2280001 seq list.txt
Output Set: N:\CRF3\07202001\I899569.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:351 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:353 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:355 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:1500 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, 5UTR LOCATION: (1)..
(282)
L:1513 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, 3UTR LOCATION:
(2794)..(6163)
L:1517 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, 3UTR LOCATION:
(2794)..(6163)
L:1521 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, CDS LOCATION: (283)..
(2793)